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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=5; day=3; hr=16; min=14; sec=47; ms=293;]
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Validated By CRFValidator v 1.0.3

Application No: 10535522   Version No: 4.0

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No. of SeqIDs Defined:	14
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<110>   Steinkasserer, Alexander

<120>   Use of Soluble Forms of CD83 and Nucleic Acids Encoding them for
        the Treatment or Prevention of Diseases

<130>   032723woJH

<140>   10535522
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<160>   14

<170>   PatentIn version 3.5

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<212>   DNA
<213>   Homo sapiens


<220>
<221>   CDS
<222>   (1)..(615)


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Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
1               5                   10                  15

gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac        96
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
            20                  25                  30

ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc       144
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
        35                  40                  45

tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag       192
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
    50                  55                  60

gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt       240
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
65                  70                  75                  80

tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac       288
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
                85                  90                  95

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg       336
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
            100                 105                 110

gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga       384
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Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
        115   120   125

tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag   432
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
    130   135   140

att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att   480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145   150   155   160

ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct   528
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
                    165   170   175

aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag   576
Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
                180   185   190

cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga   618
His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
        195   200   205

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<212>   PRT
<213>   Homo sapiens

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Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
1   5   10   15

Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
            20   25   30

Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
        35   40   45

Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
    50   55   60

Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
65   70   75   80

Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
                85   90   95

Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
                100   105   110

Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
        115   120   125

Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
        130   135   140

Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145   150   155   160

Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
                165   170   175

Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
                180   185   190

His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
                195   200   205

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<213>   Mus musculus

<220>
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<222>   (14)..(601)

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gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct   97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
        15   20   25

tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag   145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
    30   35   40

ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag   193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu
45   50   55   60

agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc   241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro
                65   70   75

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agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc        289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser
            80              85                  90

tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac        337
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn
        95                  100                 105

ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct        385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala
    110                 115                 120

aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc        433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe
125                 130                 135                 140

tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt        481
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe
                145                 150                 155

gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa        529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu
                160                 165                 170

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg        577
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val
        175                 180                 185

acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggt ttttacaaag      631
Thr Leu Pro Lys Thr Glu Thr Val
        190                 195

ccaagggcac atcagatcag tgtgcctgaa tgccacccgg acaagagaag aatgagctcc       691

atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc       751

cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct       811

ctgtggctgt cagcttaatg tttcatgtgg ctatctggtc aacctcgtga gtgctttcta       871

gtcatctaca agctatggtg agatgcaggt gaagcagggt catgggaaat ttgaacactc       931

tgagctggcc ctgtgacaga ctcctgagga cagctgtcct ctcctacatc tgggatacat       991

ctctttgaat ttgtcctgtt tcgttgcacc agcccagatg tctcacatct ggcggaaatt      1051

gacaggccaa gctgtgagcc agtgggaaat atttagcaaa taatttccca gtgcgaaggt      1111

cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc      1171

cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca      1231

catttatttt tttaatcttc atgtacttgt caaagaagaa tttttcatgt tttttcaaag      1291

aagtgtgttt ctttcctttt ttaaaatatg aaggtctagt tacatagcat tgctagctga      1351

caagcagcct gagagaagat ggagaatgtt cctcaaaata gggacagcaa gctagaagca      1411
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ctgtacagtg ccctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac      1471

aagattgtct gtatgattct ggacgagtca cttgtggttt tcactctctg gttagtaaac      1531

cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg      1591

tagtgaatac attggcaact ctactgggct gttaccttgt tgatatccta gagttctgga      1651

gctgagcgaa tgcctgtcat atctcagctt gcccatcaat ccaaacacag gaggctacaa      1711

aaaggacatg agcatggtct tctgtgtgaa ctcctcctga gaaacgtgga gactggctca      1771

gcgctttgcg cttgaaggac taatcacaag ttcttgaaga tatggaccta ggggagctat      1831

tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatttctt      1891

taatgagctg ggctccttcc tcatttgctt cccaaagaga ttttgtccca ctaatggtgt      1951

gcccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc      2011

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<212>   PRT
<213>   Mus musculus

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Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys Ala Cys Ser Leu
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Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala Cys Ser Glu Thr
            20   25   30

Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
        35   40   45

Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
    50   55   60

Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
65   70   75   80

Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
                85   90   95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
            100   105   110
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Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
        115                 120                 125


Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
    130                 135                 140


Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
145                 150                 155                 160


Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
                165                 170                 175


Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
                180                 185                 190


Thr Glu Thr Val
        195


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<213>   Artificial sequence

<220>
<223>   Synthetic primer for CD83ext

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<210>   6
<211>   31
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<220>
<223>   Synthetic primer for CD83ext

<400>   6
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<212>   DNA
<213>   Artificial sequence

<220>
<223>   Synthetic partial sequence of pGEX2ThCD83ext

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<222> (1)..(417)

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<221> mat_peptide
<222> (28)..(417)

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gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc        96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
        10              15              20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag       144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
   25              30              35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga       192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40              45              50              55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat       240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
            60              65              70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg       288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
            75              80              85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta       336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
        90              95              100

agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa       384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
   105              110              115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact       435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120              125              130


<210> 8
<211> 139
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 8

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Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
        10                  15                  20

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
    25                  30                  35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40                  45                  50                  55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
                60                  65                  70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
            75                  80                  85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
        90                  95                  100

Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
    105                 110                 115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120                 125                 130


<210>  9
<211>  435
<212>  DNA
<213>  Artificial sequence

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<223>  Synthetic partial sequence of pGEX2ThCD83ext_mut129_CtoS


<220>
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<222>  (1)..(417)

<220>
<221>  mat_peptide
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<400>  9
cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag      48
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu

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              -5                  -1  1                    5

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc         96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
         10                  15                  20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag       144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
         25                  30                  35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga       192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40                  45                  50                  55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat       240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
              60                  65                  70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg       288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
         75                  80                  85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta       336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
         90
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